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RESEARCH PAPER

Estimation of genetic variability, correlation and path analysis for yield and yield contributing characters in TM-136 × KMR(E) 16-1 F_2 population of Indian mustard [*Brassica juncea* L. (Czern and Coss)]

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Abstract: The present study was carried out to estimate the amount of genetic variability, correlation, direct and indirect effects of yield attributes on yield in F_2 population of cross combination TM-136 × KMR(E) 16-1 of Indian mustard. The experimental F_2 population was laid out during *Rabi* 2020-21 in an un-replicated trial along with parents. The observations for eleven traits were recorded for 300 F_2 progeny plants and ten plants from each parent. The range for all the traits revealed a maximum variability. High genotypic and phenotypic coefficient of variation coupled with high heritability and high genetic advance over mean were observed for the traits *viz.,* yield per plant, primary branches per plant, secondary branches per plant, racemes per plant, siliqua per raceme suggesting that these traits were controlled by additive gene action and were less influenced by environment and can be improved through simple selection. The traits, number of primary branches per plant, secondary branches per plant, racemes per plant, siliqua per raceme, siliqua length and 1000-seed weight showed a positive and significant association with the yield. The trait number of secondary branches per plant exhibited the highest direct positive effect on seed yield per plant. Hence, major emphasis may be given to these traits while developing selection strategies.

Key words: Correlation, Genetic variability, Indian mustard, Path analysis

Introduction

Historically, Brassicas are one of the earliest man-made domesticated crops. Indian mustard oil is ideal for cooking and baking. It is a common ingredient in hair oil and has medicinal properties. It is also used in the soap, lubrication, medical and tanning industries. It has pungency due to the presence of glucosinolate, which is hydrolyzed to create allylisothio-cynate that is ideal as a condiment in pickles, curries, and vegetable dishes. The mustard leaves are high in vitamin K, vitamin A, carotenes, and flavonoid antioxidants content. Despite having many uses, it received an adequate focus for genetic improvements and management only after the initiation of the technological mission in oilseeds (1986), when the country became virtually self-sufficient in edible oil (Chandel and Rao 2003). However, the demand for edible oil is growing at the rate of 3-4 per cent annually due to an ever-increasing population and an improved standard of living.

The level of genetic variations in the gene pool is a major determinant of the degree of improvement through breeding. In most Indian mustard breeding programmes, the aim is to improve the genetic potential for seed yield. The variability and heritability of the traits are the two important genetic parameters in the genetic enhancement of any trait. Mustard is a self-pollinated crop; hence varieties can be developed easily. The genetic variability present in a population can either be created by employing various methods such as hybridization or variability that is already present in the population and can be utilized through selection. In the regular course of variety development, carefully selected parents are hybridized and the population is subjected to selection and this traditional method has resulted in the development of several high-yielding varieties.

Yield is an important, complex character and it depends on several component traits and their interaction with the environment. Plant characters often interact and change in one character impacts the other. Thus, direct selection based solely on yield will not be effective to improve the trait. The correlation coefficients and path coefficients are both powerful statistical tools used to assess the relative magnitude and pattern of relationships between independent and dependent variables and examine how these variables impact yield.

Material and methods

The experimental material comprised of F_2 population of cross combination TM-136 × KMR(E) 16-1 of Indian mustard and their parents were evaluated at the Agricultural research station, Nippani, during *Rabi* 2020-21. The site of the experiment is situated in the Northern transitional zone of Karnataka at 16.2^0 N latitude and 74.2^0 E longitude at an altitude of 610 m above mean sea level. The experiment F_2 population was laid out in an un-replicated trial with their parents at a spacing of 45 x 10 cm. The observations were recorded for three hundred F_2 progeny plants along with ten plants of both the parents for eleven characters *viz*., days to first flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, racemes per plant, siliqua per raceme, seeds per siliqua, siliqua length, 1000-seed weight and yield per plant. The data analysis was done using the MS-EXCEL for estimating genetic variability and R studio for correlation and path analysis.

Result and discussion

Variability, heritability and genetic advance for yield and its attributes in F$_2$ population of TM-136 × KMR(E) 16-1

The F$_2$ population derived from cross combination TM-136 × KMR(E) 16-1 exhibited wide variability for all the traits studied (Table 1). Days to first flowering ranged from 25 to 37 days with a mean of 32 days; days to maturity ranged from 78 to 89 days with a mean of 84 days; plant height ranged from 101 to 210 cm with a mean of 152 cm; number of primary branches per plant ranged from 2 to 13 with a mean of 6 per plant; number of secondary branches per plant was ranged from 4 to 26 with a mean of 14; number of racemes per plant ranged from 10 to 39 with a mean of 20; number of siliqua per raceme ranged from 10 to 48 with a mean of 26; number of seeds per siliqua ranged from 6 to 18 with a mean of 12; siliqua length ranged from 4.00 to 7.50 cm with a mean of 5.37 cm; 1000-seed weight ranged from 3.10 to 5.80 g with a mean of 4.60 g and seed yield per plant ranged from 2.60 to 20.60 g with a mean of 8.37 g. The results revealed the presence of a large amount of variability for most of the traits under this study, suggesting a scope for selection among the individuals of the population.

The variability quantified by range includes the influence of environment and genotype × environment components. Further, the true breeding value of the genotype is precisely estimated by separating genetic variance from environmental variance. In this direction, the components of variance such as PCV and GCV were estimated. PCV and GCV estimates were high for yield per plant (46.57 % and 42.74 %) followed by primary branches per plant (33.55 % and 31.84 %), number of racemes per plant (33.54 % and 31.60 %), number of siliqua per raceme (33.49 % and 30.84 %) and number of secondary branches per plant (30.81 % and 28.83 %). Whereas, moderate PCV and GCV were recorded for seeds per siliqua (17.12 % and 15.87 %), followed by siliqua length (15.68 % and 14.59 %), plant height (11.87 % and 11.06 %) and 1000-seed weight (11.18 % and 10.49 %). Indicating a greater scope for selection to improve upon these traits. Furthermore, low PCV and GCV were observed for days to first flowering (8.71 % and 7.42 %) and days to maturity (2.63 % and 2.23 %). In the comparison of PCV and GCV estimates, it was evident that the influence of environment on the expression of most of the traits was low indicating the greater role of genetic factors causing variability in these characters. Samrath (2016), Kumar *et al.* (2013), Roy *et al.* (2015) and Ganesh (2018) also reported the same results for traits studied.

Heritability in broad sense was high for number of primary branches per plant (90.08 %), number of racemes per plant (88.76 %), 1000-seed weight (88.32 %), number of secondary branches per plant (87.56 %), plant height (86.78 %), siliqua length (86.59 %), seeds per siliqua (86.00 %), number of siliqua per raceme (84.77 %), yield per plant (84.02 %), days to first flowering (72.56 %) and days to maturity (72.02 %). Gupta *et al.* (2019) also observed the high heritability these traits. Hence, traits have been considered as major yield attributes and the presence of high heritability indicated that variability in these traits is mostly due to genetic components and is transmissible to their offspring in succeeding generation, hence selection will be more effective in further improvement of these traits (Singh *et al.,* 2011).

Genetic advance as per cent of mean (GAM) was high for seed yield per plant (80.79 %) followed by number of primary branches per plant (62.25 %), number of racemes per plant (61.33 %), number of siliqua per raceme (58.49 %), number of secondary branches per plant (55.57 %), seeds per siliqua (30.32 %), siliqua length (27.98 %), plant height (21.23 %) and 1000-seed weight (20.25 %). High heritability coupled with high GAM for these traits indicated that these traits are governed by additive gene action and selection for these traits could be effective. Thus, there is a possibility of rapid improvement for these traits. Similar results were observed by Dawar *et al.* (2018), Anjana (2016) and Somu (2001). Moderate GAM was recorded for days to first flowering (13.02 %). However, low GAM was observed for days to maturity (3.90 %). Gupta *et al.* (2019) also reported similar results for these traits.

Anjna (2016) also reported high to moderate genotypic and phenotypic coefficient of variation for traits number of secondary branches per plant, number of primary branches per plant, seed yield per plant, number of siliqua per plant, number of seeds per siliqua, siliqua length and 1000-seed weight whereas, traits *viz.* days to maturity and days to first flowering

Table 1. Variability, heritability and genetic advance as per cent of mean for yield and its attributes in F$_2$ population of TM-136 × KMR(E) 16-1.

Trait	Mean	Range		GCV (%)	PCV (%)	Heritability in broad sense (%)	GAM (%)
		Min	Max				
Days to first flowering	32.50	25.00	37	7.42	8.71	72.56	13.02
Days to maturity	83.95	78.00	89	2.23	2.63	72.02	3.90
Plant height (cm)	152.05	101.00	210	11.06	11.87	86.78	21.23
Number of primary branches per plant	6.01	2.00	13	31.84	33.55	90.08	62.25
Number of secondary branches per plant	14.26	4.00	26	28.83	30.81	87.56	55.57
Number of racemes per plant	20.27	10.00	39	31.60	33.54	88.76	61.33
Number of siliqua per raceme	26.50	10.00	48	30.84	33.49	84.77	58.49
Seeds per siliqua	12.09	6.00	18	15.87	17.12	86.00	30.32
Siliqua length (cm)	5.37	4.00	7.5	14.59	15.68	86.59	27.98
1000-seed weight (g)	4.60	3.10	5.8	10.49	11.18	88.32	20.25
Yield per plant (g)	8.37	2.60	20.6	42.74	46.57	84.02	80.79

recorded a low GCV and PCV. High to moderate heritability for seed yield per plant, plant height, number of secondary branches per plant, days to first flowering, 1000-seed weight, days to maturity, number of seeds per siliqua, siliqua per plant and siliqua length. High to moderate genetic advance was observed for the number of siliqua per plant, plant height, number of secondary branches per plant, primary branches per plant, number of seeds per siliqua and seed yield per plant in the F_2 populations of Indian mustard.

Phenotypic correlation coefficient between yield and yield attributes in F_2 population of TM-136 × KMR(E) 16-1

In F_2 population of TM-136 × KMR(E) 16-1 (Table 2), seed yield per plant recorded maximum positive significant association with secondary branches per plant (0.65) followed by number of racemes per plant (0.63), siliqua per raceme (0.57), primary branches per plant (0.54), 1000-seed weight (0.47) and siliqua length (0.19). Anjna (2016) and Acharya (2006) also indicated the strong positive association of these traits with seed yield per plant. These results indicate that individual plant selection can be practiced in F_2 and advanced segregating generations with these traits. Ganesh (2018) also observed significant correlation of seed yield with higher magnitude for traits *viz.,* number of primary branches per plant, number of secondary branches per plant, number of racemes per plant, number of siliqua per raceme and siliqua length. It is possible that linkage is responsible for these associations, *i.e.,* possessing loci on the same chromosome for the traits. Since most of the traits studied are quantitative, the correlations may also be due to sharing of some genes of the QTLs between traits, the congruency of QTL.

However, seed yield per plant showed negative significant association with days to maturity (-0.69) and days to first flowering (-0.49). Similar results were observed earlier by Gowthami *et al.* (2014) Anjna (2016), Ganesh (2018) and Kumar *et al.* (2019) indicating that selection can be practiced for these traits for the development of early maturing varieties.

Table 2. Phenotypic correlation coefficient between yield and yield attributes in F_2 population of TM-136 × KMR(E) 16-1

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
X_1	1.00	0.49**	0.03	-0.30**	-0.14*	-0.34**	-0.25**	-0.10	-0.08	-0.22**	-0.49**
X_2		1.00	0.05	-0.26**	-0.28**	-0.44**	-0.35**	-0.01	-0.18**	-0.45**	-0.69**
X_3			1.00	-0.10	-0.15*	-0.08	-0.10	0.01	0.09	-0.02	-0.12*
X_4				1.00	0.55**	0.43**	0.39**	0.07	0.02	0.23**	0.54**
X_5					1.00	0.48**	0.36**	0.09	0.05	0.26**	0.65**
X_6						1.00	0.34**	0.13*	0.10*	0.35**	0.63**
X_7							1.00	0.01	0.13*	0.26**	0.57**
X_8								1.00	0.41**	0.00	0.07
X_9									1.00	0.28**	0.19**
X_{10}										1.00	0.47**
X_{11}											1.00

* Significant at 0.05 probability level and ** Significant at 0.01 probability level.

X_1= Days to first flowering
X_2= Days to maturity
X_3= Plant height
X_4= Number of primary branches per plant
X_5= Number of secondary branches per plant
X_6= Number of racemes per plant
X_7= Number of siliqua per raceme
X_8= seeds per siliqua
X_9= siliqua length
X_{10}= 1000-seed weight
X_{11}= seed yield per plant (g)

Table 3. Direct (diagonal) and indirect effects of 10 characters on seed yield per plant at phenotypic level in bi-parental F_2 population of TM-136 × KMR(E) 16-1

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	Phenotypic correlation with seed yield
X_1	-0.1215	-0.1489	-0.0006	-0.0242	-0.0151	-0.0706	-0.0578	-0.0014	-0.0001	-0.0498	-0.49**
X_2	-0.0596	-0.3038	-0.0010	-0.0210	-0.0301	-0.0914	-0.0809	-0.0001	-0.0002	-0.1020	-0.69**
X_3	-0.0036	-0.0152	-0.0197	-0.0089	-0.0161	-0.0166	-0.0254	0.0001	0.0001	-0.0045	-0.12*
X_4	0.0365	0.0790	0.0022	0.1308	0.0591	0.0893	0.0901	0.0009	0.0001	0.0521	0.54**
X_5	0.0170	0.0851	0.0029	0.0444	0.2575	0.0997	0.0832	0.0011	0.0001	0.0589	0.65**
X_6	0.0413	0.1337	0.0016	0.0347	0.0516	0.2077	0.0786	0.0014	0.0002	0.0793	0.63**
X_7	0.0304	0.1063	0.0022	0.0315	0.0387	0.0706	0.2311	0.0001	0.0001	0.0589	0.57**
X_8	0.0134	0.0030	0.0001	0.0057	0.0097	0.0228	0.0023	0.0127	0.0004	0.0001	0.07
X_9	0.0097	0.0547	-0.0018	0.0016	0.0054	0.0208	0.0300	0.0052	0.0009	0.0634	0.19**
X_{10}	0.0267	0.1367	0.0004	0.0186	0.0280	0.0727	0.0601	0.0001	0.0002	0.1266	0.47**

* Significant at 0.05 probability level and ** Significant at 0.01 probability level.

RESIDUAL EFFECT = 0.142

X_1= Days to first flowering
X_2= Days to maturity
X_3= Plant height
X_4= Number of primary branches per plant
X_5= Number of secondary branches per plant
X_6= Number of racemes per plant
X_7= Number of siliqua per raceme
X_8= seeds per siliqua
X_9= siliqua length
X_{10}= 1000-seed weight
X_{11}= seed yield per plant (g)

In addition, a positive non-significant association was observed with seeds per siliqua (0.07) and a negative significant (-0.12) association was observed with plant height and a converse result was observed for plant height correlation with seed yield per plant by Anjna (2016), Samrath (2016) and Roy *et al.* (2015) whereas Somu (2001) and Mustafa *et al.* (2018) reported the similar results. These differences in the direction of correlation are due to the nature of the experimental material and environmental conditions in which they have been studied (Falconer, 1960).

Direct and indirect effects of characters on seed yield per plant at phenotypic level in Bi-parental F_2 population of TM-136 × KMR(E) 16-1

The path analysis (Table 3) revealed that the highest positive direct effect was exhibited by the number of secondary branches per plant (0.2575) followed by siliqua per raceme (0.2311), racemes per plant (0.2077), primary branches per plant (0.1308) and 1000-seed weight (0.1266). Hence, it would be rewarding to emphasize these traits while developing selection strategies. Furthermore, a negative direct effect was observed for traits like days to maturity (-0.3038), days to first flowering (-0.1215) and plant height (-0.0197). Roy *et al.* (2015) and Samrath (2016) also observed the positive direct effects of secondary branches per plant, siliqua per plant and 1000-seed weight on seed yield per plant. Thus, path coefficient analysis indicated that number of secondary branches per plant exhibited the highest positive direct effect on seed yield per plant followed by number of siliqua per raceme, number of racemes per plant and primary branches per plant. Hence, more emphasis should be given to these traits in the selection program to enhance the seed yield.

Conclusion

For practicing selection among the material, variability is an essential component for any trait. In the present study, a wide range of variability was observed for all the traits under consideration which indicated that the parents chosen were diverse enough. The characters *viz.* number of primary branches per plant, number of secondary branches per plant, racemes per plant, siliqua per raceme and 1000 grain weight had a positive correlation with seed yield per plant through positive direct effects. Also, these characters exhibited high heritability coupled with high genetic advance indicating the additive gene action for these traits. Further selection of these characters will improve the breeding efficiency of the population. Hence, due consideration should be given to these traits while selecting progeny plants in further generations.

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